

AMENDMENTS TO THE SPECIFICATIONIN THE WRITTEN DESCRIPTION:

Please replace the paragraph starting at page 3, line 3 with the following amended paragraph.

The present invention also provides SEQ ID NO: 2, which is a novel trehalose synthase protein with the following amino acid sequence:

Met	Ser	Ile	Pro	Asp	Asn	Thr	Tyr	Ile	Glu	Trp	Leu	Val	Ser	Gln
				5					10					15
Ser	Met	Leu	His	Ala	Ala	Arg	Glu	Arg	Ser	Arg	His	Tyr	Ala	Gly
				20					25					30
Gln	Ala	Arg	Leu	Trp	Gln	Arg	Pro	Try	Ala	Gln	Ala	Arg	Pro	Arg
				35					40					45
Asp	Ala	Ser	Ala	Ile	Ala	Ser	Val	Trp	Phe	Thr	Ala	Tyr	Pro	Ala
				50					55					60
Ala	Ile	Ile	Thr	Pro	Glu	Gly	Gly	Thr	Val	Leu	Glu	Ala	Leu	Gly
				65					70					75
Asp	Asp	Arg	Leu	Trp	Ser	Ala	Leu	Ser	Glu	Leu	Gly	Val	Gln	Gly
				80					85					90
Ile	His	Asn	Gly	Pro	Met	Lys	Arg	Ser	Gly	Gly	Leu	Arg	Gly	Arg
				95					100					105
Glu	Phe	Thr	Pro	Thr	Ile	Asp	Gly	Asn	Phe	Asp	Arg	Ile	Ser	Phe
				110					115					120
Asp	Ile	Asp	Pro	Ser	Leu	Gly	Thr	Glu	Glu	Gln	Met	Leu	Gln	Leu
				125					130					135
Ser	Arg	Val	Ala	Ala	Ala	His	Asn	Ala	Ile	Val	Ile	Asp	Asp	Ile
				140					145					150

Val	Pro	Ala	His	Thr	Gly	Lys	Gly	Ala	Asp	Phe	Arg	Leu	Ala	Glu
				155					160					165
Met	Ala	Tyr	Gly	Asp	Tyr	Pro	Gly	Leu	Tyr	His	Met	Val	Glu	Ile
				170					175					180
Arg	Glu	Glu	Asp	Trp	Glu	Leu	Leu	Pro	Glu	Val	Pro	Ala	Gly	Arg
				185					190					195
Asp	Ser	Val	Asn	Leu	Leu	Pro	Pro	Val	Val	Asp	Arg	Leu	Lys	Glu
				200					205					210
Lys	His	Tyr	Ile	Val	Gly	Gln	Leu	Gln	Arg	Val	Ile	Phe	Phe	Glu
				215					220					225
Pro	Gly	Ile	Lys	Asp	Thr	Asp	Trp	Ser	Val	Thr	Gly	Glu	Val	Thr
				230					235					240
Gly	Val	Asp	Gly	Lys	Val	Arg	Arg	Trp	Val	Tyr	Leu	His	Tyr	Phe
				245					250					255
Lys	Glu	Gly	Gln	Pro	Ser	Lue	Asn	Trp	Leu	Asp	Pro	Thr	Phe	Ala
				260					265					270
Ala	Gln	Gln	Leu	Ile	Ile	Gly	Asp	Ala	Leu	His	Ala	Ile	Asp	Val
				275					280					285
Thr	Gly	Ala	Arg	Val	Leu	Arg	Leu	Asp	Ala	Asn	Gly	Phe	Leu	Gly
				290					295					300
Val	Glu	Arg	Arg	Ala	Glu	Gly	Thr	Ala	Trp	Ser	Glu	Gly	His	Pro
				305					310					315
Leu	Ser	Val	Thr	Gly	Asn	Gln	Leu	Leu	Ala	Gly	Ala	Ile	Arg	Lys
				320					325					330
Ala	Gly	Gly	Phe	Ser	Phe	Gln	Glu	Leu	Asn	Leu	Thr	Ile	Asp	Asp
				335					340					345
Ile	Ala	Ala	Met	Ser	His	Gly	Gly	Ala	Asp	Leu	Ser	Tyr	Asp	Phe
				350					355					360

Ile	Thr	Arg	Pro	Ala	Tyr	His	His	Ala	Leu	Leu	Thr	Gly	Asp	Thr
				365					370					375
Glu	Phe	Leu	Arg	Met	Met	Leu	Arg	Glu	Val	His	Ala	Phe	Gly	Ile
				380					385					390
Asp	Pro	Ala	Ser	Leu	Ile	His	Ala	Leu	Gln	Asn	His	Asp	Glu	Leu
				395					400					405
Thr	Leu	Glu	Leu	Val	His	Phe	Trp	Thr	Leu	His	Ala	Tyr	Asp	His
				410					415					420
Tyr	His	Tyr	Lys	Gly	Gln	Thr	Leu	Pro	Gly	Gly	His	Leu	Arg	Glu
				425					430					435
His	Ile	Arg	Glu	Glu	Met	Tyr	Glu	Arg	Leu	Thr	Gly	Glu	His	Ala
				440					445					450
Pro	Tyr	Asn	Leu	Lys	Phe	Val	Thr	Asn	Gly	Val	Ser	Cys	Thr	Thr
				455					460					465
Ala	Ser	Val	Ile	Ala	Ala	Ala	Leu	Asn	Ile	Arg	Asp	Leu	Asp	Ala
				470					475					480
Ile	Gly	Pro	Ala	Glu	Val	Glu	Gln	Ile	Gln	Arg	Leu	His	Ile	Leu
				485					490					495
Leu	Val	Met	Phe	Asn	Ala	Met	Gln	Pro	Gly	Val	Phe	Ala	Leu	Ser
				500					505					510
Gly	Trp	Asp	Leu	Val	Gly	Ala	Leu	Pro	Leu	Ala	Pro	Glu	Gln	Val
				515					520					525
Glu	His	Leu	Met	Gly	Asp	Gly	Asp	Thr	Arg	Trp	Ile	Asn	Arg	Gly
				530					535					540
Gly	Tyr	Asp	Leu	Ala	Asp	Leu	Ala	Pro	Glu	Ala	Ser	Val	Ser	Ala
				545					550					555
Glu	Gly	Leu	Pro	Lys	Ala	Arg	Ser	Leu	Tyr	Gly	Ser	Leu	Ala	Glu
				560					565					570

Gln	Leu	Gln	Arg	Pro	Gly	Ser	Phe	Ala	Cys	Gln	Leu	Lys	Arg	Ile
				575					580					585
Leu	Ser	Val	Arg	Gln	Ala	Tyr	Asp	Ile	Ala	Ala	Ser	Lys	Gln	Ile
				590					595					600
Leu	Ile	Pro	Asp	Val	Gln	Ala	Pro	Gly	Leu	Leu	Val	Met	Val	His
				605					610					615
Glu	Leu	Pro	Ala	Gly	Lys	Gly	Val	Gln	Leu	Thr	Ala	Leu	Asn	Phe
				620					625					630
Ser	Ala	Glu	Pro	Val	Ser	Glu	Thr	Ile	Cys	Leu	Pro	Gly	Val	Ala
				635					640					645
Pro	Gly	Pro	Val	Val	Asp	Ile	Ile	His	Glu	Ser	Val	Glu	Gly	Asp
				650					655					660
Leu	Thr	Asp	Asn	Cys	Glu	Leu	Gln	Ile	Asn	Leu	Asp	Pro	Tyr	Glu
				665					670					675
Gly	Leu	Ala	Leu	Arg	Val	Val	Ser	Ala	Ala	Pro	Pro	Val	Ile.	
				680					685					

Please replace the paragraph starting at page 6, line 1 with the following amended paragraph.

In addition, the present invention provides SEQ ID NO: 1, which is a novel trehalose synthase gene with the following nucleotide sequence:

GATCGCTGGC	GTACTGCAGG	TAGAGCAGGC	GCATCGGCCC	CCAGGGCGCA	TCGGCCGGCT	60
CCGCTGTGCC	CTGCTGGTTC	ATGAAGCGGA	CGAAGCGGCC	ATCGCGGAAC	CGTGGACGCC	120
ATTCGGGGCT	GTCCGGGTCG	CGGCTGTCTG	TGAGCGTGCG	CCACAGGTCG	CTGCGAAACG	180
GCGGACCGCT	CCTAAGCGCG	CCGTGGATGG	GATCGCCGAG	CAGTTCGTGC	AGCTCCCAGG	240
AACGTTGCGA	ATGCAGCGCG	CCGAGGCTCA	GGCCATGCAG	ATACAGGCGC	GGTCGGCGTT	300
CGGCCGGCAG	TTCGGTCCAG	TAGCCATAGA	TCTCGGCGAA	TAGCGCGCGG	GCCACGTCGC	360

GGCCGTAGTC	GGCCTCCACC	AGCAGCGCCA	GCGGGCTGTT	CAGATAGGAG	TACTGCAACG	420
CCACGCTGGC	GATATCGCCG	TGGTGCAGGT	ATTCCACTGC	GTTTCATCGCC	GCCGGGTCTGA	480
TCCAGCCGGT	ACCGGTGGGC	GTCACCAGCA	CCAGCACCGA	TCGCTCGAAG	GCGCCGCTGC	540
GCTGCAGCTC	GCGCAAGGCC	AGACGCGCCC	GCTGGCGCGG	GGTCTCTGCC	GCGCGCAGAC	600
CGACGTAGAC	GCGAATCGGC	TCGAGCGCCG	AGCGGCCGCT	CAAGACGCTG	ATATCCGCCG	660
CCGACGGGCC	GGAGCCGATG	AACTCGCGGC	CGGTGCGGCC	CAGCTCCTCC	CAGCGCAGCA	720
ACGAGGCCCG	GCTGCCGCTT	TTCAGCGGCG	AGGCCGGTGG	CGCCGTCTCC	GGTTCGATCA	780
GGGCGTCGTA	CTGCGCGAAG	GATGCGTCCA	GCATGCGCAG	TGCCCCGCGC	GCCAGCACAT	840
CGCTGAGCAG	CGACCAGAAC	AGCGCCAGCG	CCACCAGCAC	GCCGATCACG	TTGGCCAGGC	900
GCCGTGGCAG	CACGCGGTGC	GCGTGCCGCG	AGACGAAGCG	CGACACCAGC	CGATACAGAC	960
GCGCCAGCGT	CAGCAGGATG	AGAAAGGTCG	CCAGCGCGGT	GAGAATGACT	TCGAGCAGGT	1020
GCGCACTGCT	CACCGGCGGC	ATGCCCATCA	GCGCGCGTAC	CGCGTTCTGC	CAGCCGGCGA	1080
CCTGGCTGAG	GAAATACCCG	GCCAGCAGCA	GGCAGCCGAC	CGCGATCAGC	AGATTGACCC	1140
GCTCGCGCTG	CCAGCCTGGG	CGCTCCGGCA	GTTCCAGATA	GCGCCACAGC	CAGCGCCAGA	1200
ACACGCCGAG	GCCATAGCCC	ACCGCCAGCG	CCGCGCCGGC	CAGCACGCCC	TGGCTCAGCG	1260
TCGAGCGCGG	CAGCAGCGAT	GGCGTCAGCG	CCGCGCAGAA	GAACAGCGTG	CCCAGCAGCA	1320
GGCCGAAACC	GGACAGCGAG	CGCCAGATAT	AGAGGACGGG	CAGGTGCAGC	ATGAAGATCT	1380
CCGCGGTCCG	GTGACGGCGT	CGCGCCTCGG	CATATCGAGG	CGTGTCCGGT	CGTGCGGTTC	1440
CCGTGATGGT	CCGCAGCAGG	CCAATCCGAT	GCAACGATGG	CCGAGCGGCC	GACTCAAACG	1500
TCTACATTTC	CCTAGTGCTG	CCGGAACCGA	TCGCCG			1536

ATG	AGC	ATC	CCA	GAC	AAC	ACC	TAT	ATC	GAA	TGG	CTG	GTC	AGC	CAG	TCC	1584
Met	Ser	Ile	Pro	Asp	Asn	Thr	Tyr	Ile	Glu	Trp	Leu	Val	Ser	Gln	Ser	
ATG	CTG	CAT	GCG	GCC	CGC	GAG	CGG	TCG	CGT	CAT	TAC	GCC	GGC	CAG	GCG	1632
Met	Leu	His	Ala	Ala	Arg	Glu	Arg	Ser	Arg	His	Tyr	Ala	Gly	Gln	Ala	
CGT	CTC	TGG	CAG	CGG	CCT	TAT	GCC	CAG	GCC	CGC	CCG	CGC	GAT	GCC	AGC	1680
Arg	Leu	Trp	Gln	Arg	Pro	Try	Ala	Gln	Ala	Arg	Pro	Arg	Asp	Ala	Ser	
GCC	ATC	GCC	TCG	GTG	TGG	TTC	ACC	GCC	TAT	CCG	GCG	GCC	ATC	ATC	ACG	1728
Ala	Ile	Ala	Ser	Val	Trp	Phe	Thr	Ala	Tyr	Pro	Ala	Ala	Ile	Ile	Thr	
CCG	GAA	GGC	GGC	ACG	GTA	CTC	GAG	GCC	CTC	GGC	GAC	GAC	CGC	CTC	TGG	1776
Pro	Glu	Gly	Gly	Thr	Val	Leu	Glu	Ala	Leu	Gly	Asp	Asp	Arg	Leu	Trp	
AGT	GCG	CTC	TCC	GAA	CTC	GGC	GTG	CAG	GGC	ATC	CAC	AAC	GGG	CCG	ATG	1824
Ser	Ala	Leu	Ser	Glu	Leu	Gly	Val	Gln	Gly	Ile	His	Asn	Gly	Pro	Met	
AAG	CGT	TCC	GGT	GGC	CTG	CGC	GGA	CGC	GAG	TTC	ACC	CCG	ACC	ATC	GAC	1872
Lys	Arg	Ser	Gly	Gly	Leu	Arg	Gly	Arg	Glu	Phe	Thr	Pro	Thr	Ile	Asp	

GGC Gly	AAC Asn	TTC Phe	GAC Asp	CGC Arg	ATC Ile	AGC Ser	TTC Phe	GAT Asp	ATC Ile	GAC Asp	CCG Pro	AGC Ser	CTG Leu	GGG Gly	ACC Thr	1920
GAG Glu	GAG Glu	CAG Gln	ATG Met	CTG Leu	CAG Gln	CTC Leu	AGC Ser	CGG Arg	GTG Val	GCC Ala	GCG Ala	GCG Ala	CAC His	AAC Asn	GCC Ala	1968
ATC Ile	GTC Val	ATC Ile	GAC Asp	GAC Asp	ATC Ile	GTG Val	CCG Pro	GCA Ala	CAC His	ACC Thr	GGC Gly	AAG Lys	GGT Gly	GCC Ala	GAC Asp	2016
TTC Phe	CGC Arg	CTC Leu	GCG Ala	GAA Glu	ATG Met	GCC Ala	TAT Tyr	GGC Gly	GAC Asp	TAC Tyr	CCC Pro	GGG Gly	CTG Leu	TAC Tyr	CAC His	2064
ATG Met	GTG Val	GAA Glu	ATC Ile	CGC Arg	GAG Glu	GAG Glu	GAC Asp	TGG Trp	GAG Glu	CTG Leu	CTG Leu	CCC Pro	GAG Glu	GTG Val	CCG Pro	2112
GCC Ala	GGG Gly	CGT Arg	GAT Asp	TCG Ser	GTC Val	AAC Asn	CTG Leu	CTG Leu	CCG Pro	CCG Pro	GTG Val	GTC Val	GAC Asp	CGG Arg	CTC Leu	2160
AAG Lys	GAA Glu	AAG Lys	CAC His	TAC Tyr	ATC Ile	GTC Val	GGC Gly	CAG Gln	CTG Leu	CAG Gln	CGG Arg	GTG Val	ATC Ile	TTC Phe	TTC Phe	2208
GAG Glu	CCG Pro	GGC Gly	ATC Ile	AAG Lys	GAC Asp	ACC Thr	GAC Asp	TGG Trp	AGC Ser	GTC Val	ACC Thr	GGC Gly	GAG Glu	GTC Val	ACC Thr	2256
GGG Gly	GTC Val	GAC Asp	GGC Gly	AAG Lys	GTG Val	CGT Arg	CGC Arg	TGG Trp	GTC Val	TAT Tyr	CTG Leu	CAC His	TAC Tyr	TTC Phe	AAG Lys	2304
GAG Glu	GGC Gly	CAG Gln	CCG Pro	TCG Ser	CTG Leu	AAC Asn	TGG Trp	CTC Leu	GAC Asp	CCG Pro	ACC Thr	TTC Phe	GCC Ala	GCG Ala	CAG Gln	2352
CAG Gln	CTG Leu	ATC Ile	ATC Ile	GGC Gly	GAT Asp	GCG Ala	CTG Leu	CAC His	GCC Ala	ATC Ile	GAC Asp	GTC Val	ACC Thr	GGC Gly	GCC Ala	2400
CGG Arg	GTG Val	CTG Leu	CGC Arg	CTG Leu	GAC Asp	GCC Ala	AAC Asn	GGC Gly	TTC Phe	CTC Leu	GGC Gly	GTG Val	GAA Glu	CGG Arg	CGC Arg	2448
GCC Ala	GAG Glu	GGC Gly	ACG Thr	GCC Ala	TGG Trp	TCG Ser	GAG Glu	GGC Gly	CAC His	CCG Pro	CTG Leu	TCC Ser	GTC Val	ACC Thr	GGC Gly	2496
AAC Asn	CAG Gln	CTG Leu	CTC Leu	GCC Ala	GGG Gly	GCG Ala	ATC Ile	CGC Arg	AAG Lys	GCC Ala	GGC Gly	GGC Gly	TTC Phe	AGC Ser	TTC Phe	2544
CAG Gln	GAG Glu	CTG Leu	AAC Asn	CTG Leu	ACC Thr	ATC Ile	GAT Asp	GAC Asp	ATC Ile	GCC Ala	GCC Ala	ATG Met	TCC Ser	CAC His	GGC Gly	2592
GGG Gly	GCC Ala	GAT Asp	CTG Leu	TCC Ser	TAC Tyr	GAC Asp	TTC Phe	ATC Ile	ACC Thr	CGC Arg	CCG Pro	GCC Ala	TAT Tyr	CAC His	CAT His	2640
GCG Ala	TTG Leu	CTC Leu	ACC Thr	GGC Gly	GAT Asp	ACC Thr	GAA Glu	TTC Phe	CTG Leu	CGC Arg	ATG Met	ATG Met	CTG Leu	CGC Arg	GAA Glu	2688
GTG Val	CAC His	GCC Ala	TTC Phe	GGC Gly	ATC Ile	GAC Asp	CCG Pro	GCG Ala	TCA Ser	CTG Leu	ATC Ile	CAT His	GCG Ala	CTG Leu	CAG Gln	2736
AAC Asn	CAT His	GAC Asp	GAG Glu	TTC Leu	ACC Thr	CTG Leu	GAG Glu	CTG Leu	GTG Val	CAC His	TTC Phe	TGG Trp	ACG Thr	CTG Leu	CAC His	2784
GCC Ala	TAC Tyr	GAC Asp	CAT His	TAC Tyr	CAC His	TAC Tyr	AAG Lys	GGC Gly	CAG Gln	ACC Thr	CTG Leu	CCC Pro	GGC Gly	GGC Gly	CAC His	2832
CTG Leu	CGC Arg	GAA Glu	CAT His	ATC Ile	CGC Arg	GAG Glu	GAA Glu	ATG Met	TAC Tyr	GAG Glu	CGG Arg	CTG Leu	ACC Thr	GGC Gly	GAA Glu	2880

CAC His	GCG Ala	CCG Pro	TAC Tyr	AAC Asn	CTC Leu	AAG Lys	TTC Phe	GTC Val	ACC Thr	AAC Asn	GGG Gly	GTG Val	TCC Ser	TGC Cys	ACC Thr	2928
ACC Thr	GCC Ala	AGC Ser	GTG Val	ATC Ile	GCC Ala	GCG Ala	GCG Ala	CTT Leu	AAC Asn	ATC Ile	CGT Arg	GAT Asp	CTG Leu	GAC Asp	GCC Ala	2976
ATC Ile	GGC Gly	CCG Pro	GCC Ala	GAG Glu	GTG Val	GAG Glu	CAG Gln	ATC Ile	CAG Gln	CGT Arg	CTG Leu	CAT His	ATC Ile	CTG Leu	CTG Leu	3024
GTG Val	ATG Met	TTC Phe	AAT Asn	GCC Ala	ATG Met	CAG Gln	CCC Pro	GGC Gly	GTG Val	TTC Phe	GCC Ala	CTC Leu	TCC Ser	GGC Gly	TGG Trp	3072
GAT Asp	CTG Leu	GTC Val	GGC Gly	GCC Ala	CTG Leu	CCG Pro	CTG Leu	GCG Ala	CCC Pro	GAG Glu	CAG Gln	GTC Val	GAG Glu	CAC His	CTG Leu	3120
ATG Met	GGC Gly	GAT Asp	GGC Gly	GAT Asp	ACC Thr	CGC Arg	TGG Trp	ATC Ile	AAT Asn	CGC Arg	GGC Gly	GGC Gly	TAT Tyr	GAC Asp	CTC Leu	3168
GCC Ala	GAT Asp	CTG Leu	GCG Ala	CCG Pro	GAG Glu	GCG Ala	TCG Ser	GTC Val	TCC Ser	GCC Ala	GAA Glu	GGC Gly	CTG Leu	CCC Pro	AAG Lys	3216
GCC Ala	CGC Arg	TCG Ser	CTG Leu	TAC Tyr	GGC Gly	AGC Ser	CTG Leu	GCC Ala	GAG Glu	CAG Gln	CTG Leu	CAG Gln	CGG Arg	CCA Pro	GGC Gly	3264
TCC Ser	TTC Phe	GCC Ala	TGC Cys	CAG Gln	CTC Leu	AAG Lys	CGC Arg	ATC Ile	CTC Leu	AGC Ser	GTG Val	CGC Arg	CAG Gln	GCC Ala	TAC Tyr	3312
GAC Asp	ATC Ile	GCT Ala	GCC Ala	AGC Ser	AAG Lys	CAG Gln	ATC Ile	CTG Leu	ATT Ile	CCG Pro	GAT Asp	GTG Val	CAG Gln	GCG Ala	CCG Pro	3360
GGA Gly	CTC Leu	CTG Leu	GTG Val	ATG Met	GTC Val	CAC His	GAG Glu	CTG Leu	CCT Pro	GCC Ala	GGC Gly	AAG Lys	GGC Gly	GTG Val	CAG Gln	3408
CTC Leu	ACG Thr	GCA Ala	CTG Leu	AAC Asn	TTC Phe	AGC Ser	GCC Ala	GAG Glu	CCG Pro	GTC Val	AGC Ser	GAG Glu	ACC Thr	ATC Ile	TGC Cys	3456
CTG Leu	CCC Pro	GGC Gly	GTG Val	GCG Ala	CCC Pro	GGC Gly	CCG Pro	GTG Val	GTG Val	GAC Asp	ATC Ile	ATT Ile	CAC His	GAG Glu	AGT Ser	3504
GTG Val	GAG Glu	GGC Gly	GAC Asp	CTC Leu	ACC Thr	GAC Asp	AAC Asn	TGC Cys	GAG Glu	CTG Leu	CAG Gln	ATC Ile	AAC Asn	CTC Leu	GAC Asp	3552
CCG Pro	TAC Tyr	GAG Glu	GGG Gly	CTT Leu	GCC Ala	CTG Leu	CGT Arg	GTG Val	GTG Val	AGC Ser	GCC Ala	GCG Ala	CCG Pro	CCG Pro	GTG Val	3600
ATC Ile	TGA	GCGC														3610
	CCTCTTCGCG	CGCCCCGGGT	CCGCCGCTAT	AGTGCGCAGC	GCCTGGGGCG	CGCATTGCCC										3670
	TCGCCGTCTGA	GACCAGCCCCG	TGTCGTTCAC	TTCGCTTTTC	CGCCTTGCGC	TGCTGCCGCT										3730
	GGCGTGCTTT	GCCGCACCCCG	TCTGGGCGCA	GACCGCCTGC	CCGCCCGGCC	AGCAGCCGAT										3790
	CTGCCTGAGC	GGCAGCTGCC	TCTGCGTGCC	GGCCGCCGCC	AGCGATCCAC	AGGCGGTCTA										3850
	CGACCGCGTC	CAGCGTATGG	CTACGCTGGC	CCTGCAGAAC	TGGATCCAGC	AGTCGCGCGA										3910
	CCGCCTGATG	GCCGGCGGCG	TCGAGCCGAT	ACCGCTGCAC	ATCCGCTCGC	AGCTCGAGCC										3970
	GTATTTTCGAT	CTTGCCGTGC	TGGAGAGTGC	GCGGTACCGC	GTCGGCGACG	AGGTGGTGCT										4030
	GACTGCCGGC	AACACCCTGC	TGCGCAACCC	GGACGTCAAT	GCCGTGACCC	TGATCGACGT										4090

CATCGTCTTC	CGCCACGAGG	AGGATGCCCCG	GGACAACGTC	GCGCTCTGGG	CCCATGAGCT	4150
CAAGCACGTC	GAGCAATATC	TGGACTGGGG	CGTCGCCGAG	TTCGCCCCGC	GCTATACGCA	4210
GGATTTCCGT	GCCGTGGAGC	GCCCCGCCCTA	TGCGCTGGAG	CGTGAGGTGG	AAGAGGCCCT	4270
GCGCGAGACG	CAGACGCGGC	GCTGAGCGAG	CTGATCGGTG	CTGCTGCCCCG	CACTGGG CTG	4330
AAGCCCACCA	ATGACGCCGG	CGAAAACGAA	AAACCCCGCC	GAGGCGGGGT	TTCTGACGCG	4390
GGTTGTGCGG	TCAGCTCAGA	ACGCCGGGAC	CACGGCGCCC	TTGTACTTTT	CCTCGATGAA	4450
CTGGCGTACT	TGCTCGCTGT	GCAGCGCGGC	AGCCAGTTTC	TGCATGGCAT	CGCTGTCCTT	4510
GTTGTCCGGA	CGGGCGACCA	GAATGTTTAC	GTATGGCGAG	TCGCTGCCCT	CGATCACCAG	4570
GGCGTCCTGG	GTCGGGTTCA	GCTTGGCTTC	CAGCGCGTAG	TTGGTGTGTA	TCAGCGCCAG	4630
GTCGACCTGG	GTCAGCACGC	GCGGCAGAGT	CGCGGCTTCC	AGTTCGCGGA	TCTTGATCTT	4690
CTTCGGGTTT	TCGGCGATGT	CTTCGGCGTG	GCGGTGATGC	CGGCGCCGTC	CTTCAGACCG	4750
ATC						4753

Please replace the paragraph starting at page 9, line 31 with the following amended paragraph.

Figure 1 shows an analysis of saccharides by thin-layer chromatography to which a reaction solution containing sonicated liquid from *Pseudomonas stutzeri* CJ38 and maltose solution was subjected. The symbols G, M and T indicate glucose, maltose and trehalose, respectively. In the first lane of the gel shown in figure 1 is a control containing glucose, maltose and trehalose.